

FORM PTO-1390 (Modified)
(REV 11-98)

U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

ATTORNEY'S DOCKET NUMBER

TRANSMITTAL LETTER TO THE UNITED STATES

147-201P

DESIGNATED/ELECTED OFFICE (DO/EO/US)

U.S. APPLICATION NO. (IF KNOWN, SEE 37 CFR

CONCERNING A FILING UNDER 35 U.S.C. 371

09/555971

INTERNATIONAL APPLICATION NO.

INTERNATIONAL FILING DATE

PRIORITY DATE CLAIMED

PCT/EP98/07909

4 December 1998

5 December 1997 and 12 December 1997

TITLE OF INVENTION

METHOD FOR IDENTIFYING NUCLEIC ACIDS BY ELECTRO-SPRAY MASS SPECTROMETRY

APPLICANT(S) FOR DO/EO/US

GUT, Ivo Glynne; BERLIN, Kurt; and LEHRACH, Hana

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☒ This is an express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371 (c) (2))
 - a. ☒ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☒ has been transmitted by the International Bureau.
 - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☐ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. ☒ A copy of the International Search Report (PCT/ISA/210).
8. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371 (c)(3))
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
9. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
10. ☐ An oath or declaration of the inventor(s) (35 U.S.C. 371 (c)(4)).
11. ☐ A copy of the International Preliminary Examination Report (PCT/IPEA/409).
12. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371 (c)(5)).

Items 13 to 20 below concern document(s) or information included:

13. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
14. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
15. ☐ A **FIRST** preliminary amendment.
16. ☐ A **SECOND** or **SUBSEQUENT** preliminary amendment.
17. ☐ A substitute specification.
18. ☐ A change of power of attorney and/or address letter.
19. ☒ Certificate of Mailing by Express Mail
20. ☒ Other items or information:

Six (6) sheets of drawings

U.S. APPLICATION NO. (IF KNOWN, SEE 37 CFR

09/555971

INTERNATIONAL APPLICATION NO.

PCT/EP98/07909

ATTORNEY'S DOCKET NUMBER

147-201P

21. The following fees are submitted:.

BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)) :

- ☐ Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO \$970.00
- ☒ International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO \$840.00
- ☐ International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO \$690.00
- ☐ International preliminary examination fee paid to USPTO (37 CFR 1.482) but all claims did not satisfy provisions of PCT Article 33(1)-(4) \$670.00
- ☐ International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4) \$96.00

ENTER APPROPRIATE BASIC FEE AMOUNT =**\$840.00**

Surcharge of **\$130.00** for furnishing the oath or declaration later than ☐ 20 ☒ 30 months from the earliest claimed priority date (37 CFR 1.492 (e)).

\$130.00

CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE
Total claims	21 - 20 =	1	x \$18.00
Independent claims	1 - 3 =	0	x \$78.00

\$18.00**\$0.00**

Multiple Dependent Claims (check if applicable).

☒**\$260.00****TOTAL OF ABOVE CALCULATIONS =****\$1,248.00**

Reduction of 1/2 for filing by small entity, if applicable. Verified Small Entity Statement must also be filed (Note 37 CFR 1.9, 1.27, 1.28) (check if applicable).

☐**\$0.00****SUBTOTAL =****\$1,248.00**

Processing fee of **\$130.00** for furnishing the English translation later than ☐ 20 ☒ 30 months from the earliest claimed priority date (37 CFR 1.492 (f)).

\$130.00**TOTAL NATIONAL FEE =****\$1,378.00**

Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31) (check if applicable).

☐**\$0.00****TOTAL FEES ENCLOSED =****\$1,378.00**

Amount to be:

refunded

\$

charged

\$

☒ A check in the amount of **\$1,378.00** to cover the above fees is enclosed.

☐ Please charge my Deposit Account No. _____ in the amount of _____ to cover the above fees.
A duplicate copy of this sheet is enclosed.

☒ The Commissioner is hereby authorized to charge any fees which may be required, or credit any overpayment to Deposit Account No. **02-2448** A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

BIRCH, STEWART, KOLASCH & BIRCH, LLP
P.O. Box 747
Falls Church, VA 22040-0747

SIGNATURE

Leonard R. Svensson

NAME

30,330

REGISTRATION NUMBER

5 June 2000

DATE

STATEMENT CLAIMING SMALL ENTITY STATUS
(37 CFR 1.9(f) & 1.27(d))--NONPROFIT ORGANIZATION

Docket No. _____

Applicant, Patentee, or Identifier: Ivo Glynne GUT et al.
 Application No.: 09/555,971
 Application Filed:
 International Application No.: PCT/EP98/07909
 International Filing Date: December 4, 1998
 Title: Method for Identifying Nucleic Acids by Electro-Spray Mass Spectrometry

I hereby state that I am an official empowered to act on behalf of the nonprofit organization identified below:

NAME OF NONPROFIT ORGANIZATION: **Max-Planck-Gesellschaft zur Förderung der Wissenschaften e.V.**
 ADDRESS OF NONPROFIT ORGANIZATION: **Berlin, Germany**

TYPE OF NONPROFIT ORGANIZATION:

- ☐ UNIVERSITY OR OTHER INSTITUTION OF HIGHER EDUCATION
☐ TAX EXEMPT UNDER INTERNAL REVENUE SERVICE CODE (26 U.S.C. 501(a) and 501(c)(3))
☐ NONPROFIT SCIENTIFIC OR EDUCATIONAL UNDER STATUTE OF STATE OF THE UNITED STATES OF AMERICA
 (NAME OF STATE _____)
 (CITATION OF STATUTE _____)
☒ WOULD QUALIFY AS TAX EXEMPT UNDER INTERNAL REVENUE SERVICE CODE (26 U.S.C. 501(a) and 501(c)(3))
 IF LOCATED IN THE UNITED STATES OF AMERICA
☐ WOULD QUALIFY AS NONPROFIT SCIENTIFIC OR EDUCATIONAL UNDER STATUTE OF STATE OF THE UNITED
 STATES OF AMERICA IF LOCATED IN THE UNITED STATES OF AMERICA
 (NAME OF STATE _____)
 (CITATION OF STATUTE _____)

I hereby state that the nonprofit organization identified above qualifies as a nonprofit organization as defined in 37 CFR 1.9(e) for purposes of paying reduced fees to the United States Patent and Trademark Office regarding the invention described in:

- ☐ the specification filed herewith with title as listed above.
☒ the application identified above.
☐ the patent identified above.

I hereby state that rights under contract or law have been conveyed to and remain with the nonprofit organization regarding the above identified invention. If the rights held by the nonprofit organization are not exclusive, each individual, concern, or organization having rights in the invention must file separate statements as to their status as small entities and that no rights to the invention are held by any person, other than the inventor, who would not qualify as an independent inventor under 37CFR 1.9(c) if that person made the invention, or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e).

Each person, concern, or organization having any rights in the invention is listed below:

- ☐ no such person, concern, or organization exists.
☒ each such person, concern, or organization is listed below.

Epigenomics GmbH
Kastanienallee 24
10435 Berlin, Germany

(small business concern)

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b))

NAME OF PERSON SIGNING Christa Herzog
 TITLE IN ORGANIZATION OF PERSON SIGNING Head of patent department
 ADDRESS OF PERSON SIGNING: Hofgartenstr. 8, 80539 München

SIGNATURE Christa Herzog DATE 5.10.2000
 Christa Herzog

00447 "T465560

Max-Planck-Gesellschaft zur
Förderung der Wissenschaften e.V.
Our. ref.: B 3366 PCT

Method for the identification of nucleic acid by means of electrospray mass spectrometry

The present invention relates to a method for detecting a nucleotide sequence in a nucleic acid molecule by means of predetermined probes with different masses each using electrospray mass spectrometry. Advantageously, the method of the invention allows at the same time for the characterisation of a variety of unknown nucleic acid molecules with a set of different probes. Moreover, this invention relates to a kit containing the probes and/or a probe support, optionally with nucleic acid molecules attached thereto.

The exact characterisation of nucleic acids is very time-consuming and expensive. It is possible to characterise an unknown DNA by sequencing it. This is the most precise way to analyse DNA. Sequencing of DNA, however, is very time-consuming and only necessary if the whole sequence is of interest. Only very short DNA segments (<1000 nucleobases) may be sequenced in one working process. If DNA fragments of more than 1000 nucleobases in length are to be sequenced on a large scale, it is necessary to subdivide the DNA, which makes the method more expensive.

Many statements, however, can also be made with a lower resolution. Yet, the methods that have been described up to now have the disadvantage that it might be necessary to use radioactivity and that only one probe can be used in one analysis. Such a method according to the state of the art, for instance, involves searching for partial information with an array of different target DNAs. An array of many thousands of target DNAs may be immobilized on a solid phase and subsequently, all target DNAs may be analysed together for the presence of a sequence by means of a probe (nucleic acid with a complementary sequence)^{1,2}. A match of the target DNA with the probe can be proven by hybridizing the two nucleic acids. Probes may be any nucleic acid sequences of different lengths. There are different methods for selecting optimal libraries of probe sequences that overlap only to a very small extent^{3,4}. It is also possible to compile the probe sequences purposefully in order to find certain target DNA sequences. Oligofingerprinting is an approach which uses this

technology. A library of target DNAs is scanned with short nucleic acid probes, with the probes mostly having a length of only 8-12 bases. One probe each is hybridized at once to a target DNA library that is immobilized on a nylon membrane. The probe is radioactively labelled and the hybridization is estimated according to the localisation of the radioactivity. For scanning an immobilized DNA array, fluorescently marked probes have also been used⁵. A similar method has been used for multiplexing the sequencing of DNA^{6,7}. Use is made of various vector systems for cloning target sequences. One clone each is pooled by each cloning vector, the sequencing reaction is carried out and the fragments are separated on the gel and the gel is blotted onto a nylon membrane. The different sequences of the cloning system are subsequently hybridized to the immobilized DNA, so that the sequence belonging to the respective cloning system is obtained. Hereby, the scanning of the cloning system can also be carried out by means of a probe which is detectable by mass spectrometry⁸.

Any molecules capable of interacting sequence-specifically with a target DNA can be used as probes. Oligodeoxyribonucleotides are most commonly used. For this purpose, however, any modification of nucleic acids, e.g. peptide nucleic acids (PNA)^{9,10}, phosphorothioate oligonucleotides or methyl phosphonate oligonucleotides, are suitable. The specificity of a probe is extremely important. Phosphorothioate oligonucleotides are not particularly preferred as their structure is modified by the sulphur atoms, which has a negative influence on the nature of the hybridization. This can be due to the fact that phosphorothioate oligonucleotides are usually not synthesized free of diastereomers. In the past, there has been a similar purity problem with methyl phosphonate oligonucleotides, but these oligonucleotides are increasingly synthesized free of diastereomers. An essential difference between methyl phosphonate oligonucleotides and phosphorothioate oligonucleotides is the uncharged backbone of the former, which leads to a reduced hybridization dependency on buffer salts and, all in all, to a higher affinity due to reduced rejection. Peptide nucleic acids also have an uncharged backbone which, at the same time, drastically deviates in its chemical properties from the common sugar phosphate structure of the backbone of nucleic acids. The backbone of a PNA has an amide sequence instead of a sugar phosphate backbone of normal DNA. PNA hybridizes very well to a sequence complementary to DNA. The melting temperature of a PNA/DNA hybrid is higher than the one of the corresponding DNA/DNA hybrid and the hybridization dependency on buffer salts is, again, relatively small. Electrospray mass spectrometry (ESI) is a new, very efficient method for analysing biomolecules (Meng, C.K., Mann, M. und Fenn, J.B., *Z. Phys. D.* 1988, 10, 361-368; Siuzdak, G. *Proc. Natl. Acad. Sci. USA*, 1994, 91, 11290-11297). The basic features of this

method are that a solution of a mixture of biomolecules is conducted through a metallic needle to which a high voltage is applied (typically several kilovolts), into the vacuum of a mass spectrometer. Due to the electric instability and the decreasing pressure, the solution disperses in small drips, each carrying electric charge on their surfaces. In several skimming steps, the drips are transferred to the high vacuum of the mass spectrometer. Thereby, the solvent of the drips is gradually lost and the naked, multiply charged biomolecules are located in an unfragmented form in the high vacuum of the mass spectrometer. For these methods, there are several possibilities as regards the step which comprises the mass spectrometrical analysis. One possibility relates to the separation of molecules with different mass and charge by means of a magnet (sector, quadrupole); another one relates to the analysis by means of measuring the time of flight. Hereby, the beam potential is pulsed vertically to the ion beam and the size of the particles is determined according to the time of flight. With these two embodiments it is possible to achieve an isotope resolution in the mass range of several thousand daltons. With new nanospray sources excellent spectrums can be recorded using only a few 100 fmol material.

Up to now, the ESI has essentially been successful for the analysis of peptides (Siuzdak, G., *Proc. Natl. Acad. Sci. USA*, 1994, 91, 11290-11297) and in particular for the analysis of peptide libraries produced combinatorially it has proven to be successful (Metzger, J.W., Kepter, C., Wiesmuller, K.H. and Jung, G., *Anal. Biochem.*, 1994, 219, 261-277; Winger, B.E. and Campana, J.E., *Rapid Commun. Mass Spectrom.*, 1996, 10, 1811-1813). The analysis of nucleic acids and modified variants has so far not been taken into consideration very often (Reddy, D.M, Rieger, R.A., Torres, M.C., and Iden, C.R., *Anal. Biochem.* 1994, 220, 200-207; Potier, N., Van Dorsselaer, A., Cordier, Y. Roch, O. and Bischoff, R., *Nucleic Acids Res.*, 1994, 22, 3895-3903; Greig, M. and Griffey, R.H., *Rapid Commun. Mass Spectrom.*, 1995, 9, 97-102). Thereby, problems arose as for example the fact that nucleic acid molecules are polyanions, which triggers additional problems in the ionisation.

Combinatorial syntheses¹³, i.e. the production of substance libraries starting from a mixture of preliminary stages are conducted in a liquid as well as in a solid phase. It is mainly the combinatorial solid phase synthesis that has established itself at a very early stage since the separation of by-products is particularly easy in this case. Only the target bonds attached to supports are retained in a washing step and at the end of the synthesis, they are isolated by specifically cleaving a linker. This technique allows in a very simple way for the simultaneous synthesis of a variety of different linkings to a solid phase and thus for obtaining chemically "pure" substance libraries^{14,15,16}. Consequently, chemistry can easily access the classes of linkings which are also synthesised to a solid phase in combinatorial, conventional syntheses

	1970-1979	1980-1989	1990-1999	2000-2009	2010-2019	2020-2029	2030-2039	2040-2049	2050-2059	2060-2069	2070-2079	2080-2089	2090-2099	2100-2109	2110-2119	2120-2129	2130-2139	2140-2149	2150-2159	2160-2169	2170-2179	2180-2189	2190-2199	2200-2209	2210-2219	2220-2229	2230-2239	2240-2249	2250-2259	2260-2269	2270-2279	2280-2289	2290-2299	2300-2309	2310-2319	2320-2329	2330-2339	2340-2349	2350-2359	2360-2369	2370-2379	2380-2389	2390-2399	2400-2409	2410-2419	2420-2429	2430-2439	2440-2449	2450-2459	2460-2469	2470-2479	2480-2489	2490-2499	2500-2509	2510-2519	2520-2529	2530-2539	2540-2549	2550-2559	2560-2569	2570-2579	2580-2589	2590-2599	2600-2609	2610-2619	2620-2629	2630-2639	2640-2649	2650-2659	2660-2669	2670-2679	2680-2689	2690-2699	2700-2709	2710-2719	2720-2729	2730-2739	2740-2749	2750-2759	2760-2769	2770-2779	2780-2789	2790-2799	2800-2809	2810-2819	2820-2829	2830-2839	2840-2849	2850-2859	2860-2869	2870-2879	2880-2889	2890-2899	2900-2909	2910-2919	2920-2929	2930-2939	2940-2949	2950-2959	2960-2969	2970-2979	2980-2989	2990-2999	3000-3009	3010-3019	3020-3029	3030-3039	3040-3049	3050-3059	3060-3069	3070-3079	3080-3089	3090-3099	3100-3109	3110-3119	3120-3129	3130-3139	3140-3149	3150-3159	3160-3169	3170-3179	3180-3189	3190-3199	3200-3209	3210-3219	3220-3229	3230-3239	3240-3249	3250-3259	3260-3269	3270-3279	3280-3289	3290-3299	3300-3309	3310-3319	3320-3329	3330-3339	3340-3349	3350-3359	3360-3369	3370-3379	3380-3389	3390-3399	3400-3409	3410-3419	3420-3429	3430-3439	3440-3449	3450-3459	3460-3469	3470-3479	3480-3489	3490-3499	3500-3509	3510-3519	3520-3529	3530-3539	3540-3549	3550-3559	3560-3569	3570-3579	3580-3589	3590-3599	3600-3609	3610-3619	3620-3629	3630-3639	3640-3649	3650-3659	3660-3669	3670-3679	3680-3689	3690-3699	3700-3709	3710-3719	3720-3729	3730-3739	3740-3749	3750-3759	3760-3769	3770-3779	3780-3789	3790-3799	3800-3809	3810-3819	3820-3829	3830-3839	3840-3849	3850-3859	3860-3869	3870-3879	3880-3889	3890-3899	3900-3909	3910-3919	3920-3929	3930-3939	3940-3949	3950-3959	3960-3969	3970-3979	3980-3989	3990-3999	4000-4009	4010-4019	4020-4029	4030-4039	4040-4049	4050-4059	4060-4069	4070-4079	4080-4089	4090-4099	4100-4109	4110-4119	4120-4129	4130-4139	4140-4149	4150-4159	4160-4169	4170-4179	4180-4189	4190-4199	4200-4209	4210-4219	4220-4229	4230-4239	4240-4249	4250-4259	4260-4269	4270-4279	4280-4289	4290-4299	4300-4309	4310-4319	4320-4329	4330-4339	4340-4349	4350-4359	4360-4369	4370-4379	4380-4389	4390-4399	4400-4409	4410-4419	4420-4429	4430-4439	4440-4449	4450-4459	4460-4469	4470-4479	4480-4489	4490-4499	4500-4509	4510-4519	4520-4529	4530-4539	4540-4549	4550-4559	4560-4569	4570-4579	4580-4589	4590-4599	4600-4609	4610-4619	4620-4629	4630-4639	4640-4649	4650-4659	4660-4669	4670-4679	4680-4689
--	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------

2

combinatorial libraries has also been described several times^{19,20,21,22}.

and a bifunctional linker are used^{24,25,26}.

metal (magnetic beads). A further method for binding a target DNA is based on the

use of a short recognition sequence (e.g. 20 bases) in the target DNA for the hybridization to a surface-immobilized oligonucleotide²⁷. Enzymatic techniques for introducing chemically active positions into target DNA have also been described²⁸. In this case, a 5'-NH₂ functionalization is carried out enzymatically at a target DNA.

As has been described before, there is a number of methods known in the state of the art, which are all geared to an exact analysis of nucleic acids. Normally, these techniques are either very time-consuming and/or expensive.

Thus, the technical problem underlying the present invention was to provide a fast and cost-efficient method for the identification of target nucleic acids.

This technical problem has been solved by providing the embodiments characterised in the claims.

Therefore, the present invention relates to a method for detecting a nucleotide sequence in a nucleic acid molecule comprising the following steps:

- (a) hybridization of nucleic acid molecules to a set of probes of different nucleobase sequences, wherein each probe has a mass that differs from the one of all the other probes;
- (b) separation of the probes that were not hybridized;
- (c) detachment of a specifically hybridized probe in a solvent;
- (d) analysis of the hybridized probes in a solution by means of electrospray mass spectrometry; and
- (e) determination of the nucleic acid molecules by means of the probes hybridized to them.

Preferably, the nucleic acid molecules are fixed to a support. In this case, it is preferred that the positions of the probes on the probe support allow for an allocation to the nucleic acid molecule hybridizing therewith. The term "probe support", as used according to the invention, means any form of support material.

The method according to the invention (cf. Figure 1) advantageously combines methods for analysing target nucleic acids (oligofingerprinting), and the mass spectrometrical analysis of nucleic acids and modified nucleic acids. Thereby, a large number of different probes is used which allow for the detection of one or more nucleotide sequences in one nucleic acid molecule. So far, it has not been possible to combine these two methods, because the differences in the mass of the probes

did not allow for clear conclusions as to the sequence, and because the sensitivity of a mass spectrometric analysis of nucleic acids was not adapted to the probe amounts of an oligofingerprinting experiment. In the broadest sense of the invention, a nucleic acid molecule containing the nucleotide sequence(s) that is (are) (essentially) complementary is determined by the hybridization of a specific probe (or several specific probes). Due to this determination, it can also be proven that a specific nucleotide sequence or very similar sequences (for example in the case of a hybridization under non-stringent conditions, see below) is/are contained in the molecule. It is clear to the person skilled in the art that it is not always possible to exactly determine a nucleotide sequence searched for by means of a hybridization method since – even under stringent hybridization conditions – a hybridization of a probe might possibly take place in spite of so-called "mismatches" (for example from a certain minimum length of a probe or with positioning of the mismatch(es) that can be tolerated during hybridization). With a given nucleotide sequence of a probe, a complementary sequence in the nucleic acid molecule can only be determined with a certain estimation in some parts of the embodiments since, apart from exact complementary sequences, possibly also such sequences can be determined which are not exactly complementary in their sequences. Thus, the nucleotide sequence also comprises homologous nucleotide sequences which preferably exhibit a degree of homology of more than 90 %, particularly preferred more than 95 %. The present invention comprises all the above-mentioned embodiments.

Depending on which hybridization conditions are selected, the method of the invention may be used for detecting either specific nucleotide sequences or groups of nucleotide sequences having similar sequences. If, for instance, stringent hybridization conditions are selected, the probes used are only able to hybridize to the nucleotide sequences that are exactly complementary to their nucleobase sequences. If, however, non-stringent hybridization conditions are chosen, the probes used can detect all the nucleotide sequences that differ from the nucleobase sequences in that they still allow for hybridization under the conditions selected. In this way, the method according to the invention may also be used for detecting homologues, variants or alleles or a specific sequence. The person skilled in the art knows what stringent and non-stringent conditions are; cf. Sambrook et al., "A Laboratory Manual", CSH Press, Cold Spring Harbor, 2nd ed. 1989, Hames and Higgins (editors) "Nucleic Acid Hybridization, A Practical Approach", IRL Press, Oxford 1985. Stringent hybridization conditions are, for example, hybridization in 6 x SSC, 5 x Denhardt's reagent, 0.5 % SDS and 100 µg/ml denatured DNA at 65°C and washing in 0.1 x SSC, 0.1 % SDS at 65°C. Non-stringent hybridization conditions differ from the above-mentioned conditions insofar as, for example, hybridization and

washing are carried out at a lower temperature, e.g. at 50°C or 55°C and/or the amount of SSC is raised, for example, to 1 x or 2 x SSC.

The method of the invention also allows for the detection of several different sequences in one target DNA, wherein the different sequences may be complementary to different probes. At the very best, e.g. when using probes with overlapping sequences, the whole nucleotide sequence of a target sequence may be detected or clarified.

With the method of the invention it may first be determined whether a target nucleic acid was fixed to an immobilization support, which exhibits a sequence that can be hybridized to a probe under the conditions selected. If this is the case, the nucleic acid of the sample may be further analysed and characterised. As in the method of the invention, usually only a very small percentage of a sample has to be used for the analysis according to the invention, the nucleic acid that is not used may be further analysed with standard methods, e.g. sequencing methods.

The removal of the specifically hybridized probes in a solvent is preferably conducted by means of thermal denaturation or alkaline denaturation. In particular, aqueous solutions or mixtures of water and organic solvents are suitable solvents, provided the organic solvent can be mixed with water (e.g. water and acetonitrile). Preferably, the mixtures are used at a ratio of 1:1. As the hybridized molecules are to be denaturated, the selection of the mixture, in addition, depends on the kind of molecules that are to be hybridized.

The method according to the invention may also be carried out several times either simultaneously or consecutively, with hybridization conditions being varied. In this way, it is possible, for example, to find out at first, whether a target DNA exhibits a specific degree of homology to other target DNAs, before searching for specific sequences.

The allocation of the probe hybridized at a specific position on the probe support to the immobilized sample is preferably conducted by means of a data processing system which allocates the respective spectrum recorded at a position of the probe support to a target DNA located exactly at the same position. Preferably, the target nucleic acids are located in a specific order on the surface or on the protein support.

In a preferred embodiment of the method according to the invention, the nucleic acid molecules are transferred to the surface of a support before or after step (a). For this

In another preferred embodiment of the method of the invention, the probes used are nucleic acids having a mass tag. According to this embodiment, the probes may also have several tags which may be located at different positions, e.g. at the 5' and the 3' end. The versatility and sensitivity of the method of the invention may be increased considerably by combining the amount and the localisation of mass tags, optionally in combination with charge tags.

In a particularly preferred embodiment the mass tags are at the same time charge tags, while in another particularly preferred embodiment, the nucleic acids additionally have a charge tag (cf. Figure 2).

Charge tagging may be conducted according to the method of Gut et al.^{11,12}. An amino-functionalized substrate (1 mM) is put in trimethylamine/CO₂ buffer (pH = 8.5, 200 mM) on ice at 0°C with 1 % ω-trimethylammoniumhexanoic acid-N-hydroxy-succinimide ester (CT). After 30 minutes, the volatile buffer and the solvent in the vacuum are removed. The amino-functionalized substrate may, for example, be a combinatorially produced library of probes differing in their mass. By varying length and functionalization of the CT, the masses of the substrate library can be altered by a defined value (Fig. 2). As in the combinatorial synthesis, a probe library containing 64 probes differing in their mass in a range of 200 Da may be generated, the mass/charge tags increase the mass by units of 200 Da each, i.e. the first combinatorial synthesis preparation is generated with the smallest charge tag possible, the second with a mass/charge tag that has 200 Da more in weight, the third mass/charge tag that has another 200 Da more in weight, etc. In theory, this range can be extended at will as long as the mass spectrometer used is able to eliminate the difference between the two probes with neighbouring masses and as long as the synthesis seems to be feasible in practice. For probes with 10 nucleobases, a basic mass in the range of 2600 to 2800 Da is obtained. For mass spectrometers which can be bought at present, the range of mass that can be used and that has a sufficient accuracy as regards mass is below 4000 Da. Thus, seven ensembles of 64 probes can be used (all in all 448 probes).

The synthesis of peptides on an automated synthesizer takes place from the C-terminal end to the N-terminal end, the synthesis of nucleic acids from the 3' to the 5' end. There is the possibility of linking a primary amino function to one or to both ends in order to obtain mass shifting by means of one or two functionalizations. Alternatively, the masses of a library of combinatorially produced probes may also be altered by inserting some building blocks with a defined mass (e.g. amino acids in a combinatorial synthesis of PNAs) before inserting the combinatorial building blocks.

The first combinatorial synthesis starts directly at the support. For the second combinatorial synthesis, first of all two valines, for example, are coupled. Valine has a mass of 99 Da. With two valines the mass of the second combinatorial synthesis is changed by 198 Da compared to the first one. For the third combinatorial synthesis, first of all four valines are coupled, as a consequence, the mass of this ensemble is by 396 Da higher than the first one, etc. If a charge tag is necessary, it may be attached later on to the N-terminal end according to the above-mentioned method. It is also possible to couple the charge tags to the solid phase first and then to continue with the combinatorial synthesis (cf. for example Fig. 3).

Another possibility is to attach several fixed charges of the same polarity at the same time. Thus, the range of detection can be reduced. In a mass spectrometer, a molecule with two charges with the corresponding half of the mass is observed. This may be of advantage when the resolution of the mass spectrometer decreases drastically towards larger mass. It has been described before how to solidly link positive fixed charges to a probe. Negative fixed charges may have similar advantages. Positive and negative fixed charges can be generated with similar methods.

For the localisation, the amount and the combinatorics of the charge tags, the statements made in connection with the mass tags apply accordingly. Therefore, the sensitivity of an analysis may be improved by means of charge tagging at the 5' or 3' end of the library. This is particularly true if otherwise a neutral charge is generated by introducing alkylphosphonate groups into the non-randomized positions (cf. below). In addition, by means of mass tagging, which is inevitably related to charge tagging, the analysis of the fragments resulting from the cleavage at the phosphorothioate groups is facilitated. It is also possible to use phosphoroselenoates for achieving a preferred cleavage at certain positions.

In another preferred embodiment of the method of the invention, the probes are modified nucleic acid molecules.

In a particularly preferred embodiment, these modified nucleic acid molecules are PNAs, alkylated phosphorothioate nucleic acids or alkylphosphonate nucleic acids.

In another preferred embodiment, the probes of the method of the invention are generated by means of combinatorial solid phase synthesis. This, for example, can be carried out by means of the commonly used Boc solid phase synthesis which is also used commercially for the synthesis of PNA pure substances. In this case, all

four or more than one of the bases adenine, guanine, cytosine or thymine are incorporated next to each other in selected positions within a sequence of the probe DNA that is otherwise determined. This takes place by using not only one but several synthesis building blocks in one step of the solid phase synthesis. By varying several of these positions, a PNA library is created. After the PNA synthesis a charge tagging may be conducted at the free terminal amino function. This improves the dynamic range of the PNA analysis by means of ESI.

Therefore, in a preferred embodiment, the different building blocks for the solid phase synthesis are labelled in such a way that their mass or the mass of the probes synthesized from them can be differentiated in the mass spectrometer. This labelling is accomplished by introducing a different mass modification at the backbone in a way corresponding to the base. In this way, the synthesized probes obtain a mass that is specific to their sequences. If the probes now specifically bind to an immobilized target DNA, the information on the mass accessible in the mass spectrometrical experiment makes it possible to draw conclusions as to the sequences of the respective hybridized probe.

In another particularly preferred embodiment of the method of the invention, the building blocks are labelled with a methyl, ethyl, propyl, a branched or non-branched alkyl, a halogen-substituted branched or non-branched alkyl-or alkoxyalkyl, alkylaryl, arylalkyl, alkoxy or aryloxyalkyl group or with one of their deuterated or other isotopic variants. For, if building blocks are used the mass of which has not been modified, the molecular mass only makes it possible to draw conclusions as to the composition of the bases, but not as to the sequence, mass-labelled building blocks (i.e. PNA monomers substituted at the backbone) are used which are characteristic to any randomized position within the PNA library. As in this way the synthesis building block of a specific base has a different mass in position X than in position y, it is possible to differentiate also different sequences with the same gross composition of the bases through the molecular mass. The respective substituents are selected by numeric values in such a way that a determined mass corresponds unequivocally to any possible sequence due to the described characteristics of the library synthesis.

The synthesis of nucleic acid probe libraries is conducted at the synthesizer by inserting mixtures of different nucleoside derivatives (usually phosphoramidites) at the positions to be randomized. The libraries resulting therefrom can also be used as probes in the above-described method. In order to differentiate the different sequences within the library, a specific bond breaking at the phosphodiester bonds located at a determined side of the randomized positions is to be carried out.

Therefore, in another preferred embodiment of the method of the invention, the probes have at least one modification in a defined position away from the randomized nucleotides which allow for the cleavage of the probe.

In a particularly preferred embodiment, this modification is the introduction of a phosphorothioate group and/or an RNA base and/or a phosphodiester bond.

If a probe contains three randomized positions, at least two such bond breakings are necessary (Fig. 6). As a result, three fragments are obtained which contain one randomized position each and which thus allow for a direct conclusion as to the variable base through its mass due to the composition otherwise known. The cleavage of the described bonds may also be conducted incompletely. This makes it possible to include larger fragments to secure the sequence information or to concretize it in the case of ambiguities. The specific bond breaking at the randomized positions is carried out by introducing phosphorothioate groups already during the synthesis of the library. These may first be hydroxyalkylated with hydroxyalkylhalides and then cleaved selectively under alkaline conditions. Alternatively, the samples may be set up in such a way that uracil is inserted next to a randomized position. The backbone can then be broken at the same position by means of uracil DNA glycosylase and subsequent alkaline treatment.

The above-described principle of mass tagging for certain components in determined positions may be used for various partial libraries which then may be united to a larger library.

Therefore, in another preferred embodiment, the probes are generated as partial libraries having different masses and/or charge tags. It is necessary to mass-label also the partial libraries in their syntheses so that specific analysed masses allow for conclusions as to that specific partial library. Usefully, this is carried out through natural amino acids which are easy to attach to a PNA library in a solid phase synthesis. By means of mass-labelling different partial libraries, it is possible to considerably extend the range of mass which is disposable for the analysis of the total library.

Moreover, the present invention relates to a kit containing the probes and/or parts of an immobilization system (probe supports), optionally with the nucleic acid molecules bound. (Coated) "magnetic beads" or a (coated) microtitre plate are suitable immobilization systems. As has been described before, the surface of the

immobilization system is pretreated and thus allows for the binding of the nucleic acids. Preferably, this pretreatment is carried out in a chemical way.

In this application, a number of publications are cited which are herewith incorporated into the specification by reference.

The Figures show:

Figure 1

Scheme of fingerprinting with mass spectrometrical scanning.

1. Combinatorially generated library of probes that can be differentiated by their mass.
2. The library is hybridized to an immobilized target DNA. After washing it intensively (to remove non-specifically bound probes), the correctly hybridized probes are separated from the target DNA.
3. This solution is analysed in an electrospray mass spectrometer. The partial sequences of the target DNA are determined by clearly allocating the mass to the sequences.

Figure 2

N-terminal mass/charge tagging.

A charge tag may be introduced at the 5' of a nucleic acid or a modified version of a nucleic acid, or at the N-terminal end of a PNA. The charge tag has an N-hydroxy-succinimidester function and a quarternary ammonium group. These two functionalizations are separated by one group R_1 . R_1 is used to vary the mass of the charge tags (coupling of the charge tags is carried out at a slightly alkaline pH (8.5) in an aqueous solution on ice. The reaction is completed within 30 minutes).

Figure 3

Principle of synthesis of PNA libraries using syntheses of mass-labelled syntheses that are carried out in parallel as well as mass-labelled building blocks L (randomized position). Various bases with different substituents each are used (as mass tags) in

the randomized positions at the backbone. The mass of the respective PNA molecule is allocated unequivocally to its sequence.

Figure 4

Calculated mass spectrum of a PNA library.

Two different solid phase syntheses (one of which is mass-labelled) with 32 different sequences each make up 64 different mass peaks, each of them being allocated to a specific sequence from a PNA library with 3 variable positions with four bases (A, C, G and T being inserted). The calculation is based on the substituents listed in Table 1. For the calculations the computer programme MASP (© Dr. Christoph Steinbeck) was used.

Figure 5

Possible synthesis components for the combinatorial Boc solid phase synthesis as are also used for the synthesis of PNA libraries that can be differentiated due to their mass. The components listed in Table 1 are shown.

Figure 6

Sequence analysis of probes by means of specific bond breakings.

The different sequences of a library of DNA probes can also be identified through mass spectrometry by means of specific bond breakings at the randomized positions ($N = A, G, C \text{ or } T$). A phosphorothioate function at which the DNA may be cleaved specifically (e.g. with idoethanol) is inserted during the solid phase synthesis. This is shown schematically without taking the exact chemical nature of the fragments into account. Since the sequence is known to a great extent, the mass of the fragments makes it possible to determine the total sequence without having to carry out a complete sequencing. The substituent R_1 stands for any possible further DNA sequence, R_2 for another possible sequence or $-H$. R_3 stands for $-OH$ (phosphodiester) or alkyl- (alkylphosphonate).

The examples explain the invention.

Example 1: Explanation of an embodiment of the whole method of the invention

A target DNA is generated with a function allowing for its immobilization at a surface. The target DNA is produced by means of PCR and in said PCR, a primer functionalized with biotin is used. For the immobilization, the surface is coated with streptavidin. A library of probes that can be differentiated due to their mass is hybridized to a target DNA in the above-described way. Complementary building blocks of the probe library bind to the respective target DNAs. Then, they are washed thoroughly to remove non-specifically bound probes. The specific probes are separated from the target DNA by means of heat denaturation. The solution is analysed in an electrospray mass spectrometer. Due to the mass found and the fact that the mass of the probes is distinguishable conclusions as to partial sequences in the target DNA can be drawn.

Example 2: Analysis of target DNA immobilized via a biotin-streptavidin bridge

A target DNA is attached to a streptavidin-coated magnetic bead by means of a biotin function. A library of probes distinguishable by mass is hybridized to target DNA. Non-specific hybridizations are washed off. By heating in an aqueous solution, the specific hybridized probes are detached. The aqueous solution is analysed in an electrospray mass spectrometer. Due to the mass found and the fact that the mass of the probes is distinguishable conclusions as to partial sequences in the target DNA can be drawn.

Example 3: Immobilization of target DNA

In a preferred variant of the method, the target DNA is attached to a bead consisting of an epoxy-functionalized acrylpolymer. Subsequently, the epoxy functions that have not reacted are deactivated with a surplus of an amine. The example is continued as described in Example 2.

Example 1: Explanation of an embodiment of the whole method of the invention

A target DNA is generated with a function allowing for its immobilization at a surface. The target DNA is produced by means of PCR and in said PCR, a primer functionalized with biotin is used. For the immobilization, the surface is coated with streptavidin. A library of probes that can be differentiated due to their mass is hybridized to a target DNA in the above-described way. Complementary building blocks of the probe library bind to the respective target DNAs. Then, they are washed thoroughly to remove non-specifically bound probes. The specific probes are separated from the target DNA by means of heat denaturation. The solution is analysed in an electrospray mass spectrometer. Due to the mass found and the fact that the mass of the probes is distinguishable conclusions as to partial sequences in the target DNA can be drawn.

Example 2: Analysis of target DNA immobilized via a biotin-streptavidin bridge

A target DNA is attached to a streptavidin-coated magnetic bead by means of a biotin function. A library of probes distinguishable by mass is hybridized to target DNA. Non-specific hybridizations are washed off. By heating in an aqueous solution, the specific hybridized probes are detached. The aqueous solution is analysed in an electrospray mass spectrometer. Due to the mass found and the fact that the mass of the probes is distinguishable conclusions as to partial sequences in the target DNA can be drawn.

Example 3: Immobilization of target DNA

In a preferred variant of the method, the target DNA is attached to a bead consisting of an epoxy-functionalized acrylpolymer. Subsequently, the epoxy functions that have not reacted are deactivated with a surplus of an amine. The example is continued as described in Example 2.

Example 4: Analysis of various target DNAs in a microtitre plate

In a microtitre plate 96 or 384 different biotin-functionalized target DNAs are immobilized in one well each. In each well, hybridization to a library of probes distinguishable by mass is carried out. The plate is washed in order to remove non-specifically bound hybridizations. The specific hybridizations are solved in the respective well by heating in an aqueous solution. The aqueous solution in each well is analysed in an electrospray mass spectrometer. Due to the mass found and the fact that the mass of the probes is distinguishable allow for conclusions as to partial sequences of the target DNA in the respective well.

Example 5: Synthesis of a PNA library with 64 different sequences

Figure 4 and Table 1 show an example of a PNA library with a clear relation between mass and sequence. In an otherwise random PNA, three positions are to be varied in the combinatorial solid phase synthesis. With 4 different bases this corresponds to 64 possible linkings. In the present example, two separate syntheses are conducted with the building blocks listed in Table 1. The second synthesis is additionally mass-labelled by adding two valine units. By each synthesis 32 compounds are obtained which can all be differentiated by their mass. Both partial libraries can be united to one library containing 64 different sequences, each one with a specific mass. The 64 peaks do not overlap, each peak corresponds to a specific sequence from a PNA library with three randomized base positions (4 bases each).

Example 6: Creation of a probe library with 448 probes

7 syntheses are carried out according to the method described in the latter example and subsequently, the mass/charge tags are coupled.

	mass range
1. 64 probes: charge tag- TCP ₁ GAP ₂ GAP ₃ G	2600-2800 Da
2. 64 probes: charge tag+200 Da mass tag- TCP ₁ AGP ₂ GAP ₃ G	2800-3000 Da
3. 64 probes: charge tag+400 Da mass tag- TCP ₁ AGP ₂ AGP ₃ G	3000-3200 Da
4. 64 probes: charge tag+600 Da mass tag- TCP ₁ AAP ₂ AGP ₃ G	3200-3400 Da
5. 64 probes: charge tag+800 Da mass tag- TCP ₁ AAP ₂ GAP ₃ G	3400-3600 Da
6. 64 probes: charge tag+1000 Da mass tag- TCP ₁ GAP ₂ GAP ₃ G	3600-3800 Da

7. 64 probes: charge tag+1200 Da mass tag- TCP₁GAP₂AGP₃G 3800-4000 Da

In the above-mentioned synthesis series, the sixth synthesis serves as an internal control. Alternatively, the following synthesis may also be conducted:

6. 64 probes: charge tag+1000 Da mass tag- TCP₁GGP₂GAP₃G 3600-3800 Da.

Example 7: Coating of a microtitre plate with protein

The surface of a microtitre plate is coated with Gene32, a protein that non-specifically binds single-stranded DNA. After coating the target with this protein, an array of target DNAs can be put onto it. If the array of the target DNAs consists of cDNA, these were primed with oligo-dT (e.g. dTTTTTTTTTTTTT) in this PCR. Oligo-dT interacts heavily with Gene32. The covalent coupling of the oligo-dT to Gene32 may be achieved by means of photocrosslinking with short UV light^{29,30}. After this immobilization, a library of probes may be used for analysing the target DNA in the above-described way. Use may also be made of sequence-specific protein/DNA interaction (e.g. GCN4/AP1).

Example 8: Immobilization of target DNA at an epoxy-functionalized solid phase.

10 mg support (Eupergit C250 L, Röhm Pharma Polymere) are suspended in 1 ml immobilization buffer (1 M K₂HPO₄/KH₂PO₄, pH 7.5). 1.5 nmol of the target DNA that is to be immobilized is added and incubated for 24 hours at room temperature while shaking gently. The supernatant is removed and the epoxy functions which have not reacted are deactivated through treatment with 1 M glycine solution for 24 hours at room temperature. The supernatant is removed and the support is washed several times. In this way, the immobilized DNA can be stored for a longer time at -20°C.

Example 9: Selective hybridization with "charge tagged" PNAs

The immobilized target DNA is incubated for 15 min at 65°C with the library of "charge tagged" PNA probes (80 pmol in 20 µl/8 pmol immobilized DNA) in hybridization buffer (10 mM Tris/HCl), 5 mM NH₄Cl, 15 % formamide) and subsequently, the probes that have not been hybridized are removed by washing

three times with hybridization buffer. Then, the dehybridization is carried out in 40% acetonitril at 80°C. An aliquot of this solution is lyophilized, put into water and analysed in a ESI mass spectrometer.

base	position 1	position 2	position 3
A	H	<i>i</i> Pr	H
T	H	Me	<i>i</i> PrOCH ₂
C	H	H	<i>i</i> PrOCH ₂ *
G	H	<i>i</i> Bu	H*

Table 1: Substituents fixed at the PNA subunits for producing a mass-labelled library with an unequivocal mass/sequence.

Relation. *: second synthesis, mass-labelled with 2 valine units. Figure 5 shows the corresponding synthesis building blocks.

References

- ¹ Hoheisel, J.D. and Lehrach, H. 1993. Use of reference libraries and hybridisation fingerprint for relational genome analysis. FEBS. 325: 118-122.
- ² Scholler, P., Karger, A.E., Meier-Ewert, S., Lehrach, H., Delius, H. and Hoheisel, J.D. 1995. Fine-mapping of shotgun template-libraries; an efficient strategy for the systematic sequencing of genomic DNA. Nucleic Acids Res. 23: 3842-3849.
- ³ Brenner, S. 1994. Methods for sorting polynucleotides using oligonucleotide tags. US Patent. 5,604,097.
- ⁴ Brenner, S. 1995. Minimally cross-hybridizing sets of oligonucleotide tags. US Patent. 5,635,400.
- ⁵ Guo, Z., Guilfoyle, R.A., Thiel, A.J., Wang, R. and Smith, L.M. 1994. Direct fluorescence analysis of genetic polymorphisms by hybridization with oligonucleotides arrays of glass supports. Nucleic Acids Res. 22: 5456-5465.
- ⁶ Church, G.M. and Kieffer-Higgins, S. 1988. Multiplex DNA sequencing. Science. 240: 185-188.
- ⁷ Church, G.M. and Kieffer-Higgins, S. 1990. Multiplex analysis of DNA. US Patent. 5,149,625.
- ⁸ Arlinghaus, H.F., Kwoka, M.N., Guo, X.-Q. and Jacobson, K.B. 1997. Multiplex DNA sequencing and diagnostics by hybridization with enriched stable isotope labels. Anal. Chem. 69: 1510-1517.
- ⁹ Nielsen, P.E., Buchardt, O., Egholm, M. and Berg, R.H. 1993. Peptide nucleic acids. US Patent. 5,539,082.

- ¹⁰ Buchardt, O., Egholm, M., Berg, R.H. and Nielsen, P.E. 1993. Peptide nucleic acids and their potential applications in biotechnology. *Trends in Biotechnology*, 11: 384-386.
- ¹¹ Gut, I.G. and Beck, S. 1995. Method of nucleic acid analysis. Patent WO96/27681.
- ¹² Gut, I.G., Jeffery, W.A., Pappin, D.J.C. and Beck, S. 1997. Analysis of DNA by 'charge tagging' and matrix-assisted laser desorption/ionization mass spectrometry. *Rapid Commun. Mass Spectrom.* 11: 43-50.
- ¹³ Lowe, G. 1995. Combinatorial Chemistry. *Chem. Soc. Rev.* 24: 309.
- ¹⁴ Jung, G., Früchtel, J.S. 1996. Organische Chemie an fester Phase. *Angew. Chem.* 108: 19-46.
- ¹⁵ Choong, I.C., Ellman, J.A. 1996. Solid-Phase Synthesis: Applications to Combinatorial Libraries. *Ann. Reports in Med. Chem.* 31: 309.
- ¹⁶ Pirrung, M.C. 1997. Spatially Addressable Combinatorial Libraries. *Chem. Rev.* 97: 473.
- ¹⁷ Cook, P.D., Kiely, J. and Sprankle, K. 1994. Peptide nucleic acid combinatorial libraries and improved methods of synthesis. US Patent. 5,539,083.
- ¹⁸ Nielsen, P.E. Peptide nucleic acids: a new dimension to peptide libraries and aptamers. *Methods in Enzymology.* 426-433.
- ¹⁹ Metzger, J.W., Stevanovic, S., Brünjes, J., Wiesmüller, K.-H., Jung, G. 1994. Electrospray Mass Spectrometry and Multiple Sequence Analysis of Synthetic Peptide Libraries. *Methods: A Companion to Methods in Enzymology* 6: 425-431.
- ²⁰ Loo, J.A., DeJohn, D.E., Andrews, P.C. 1996. Application of Mass Spectrometry for Characterizing and Identifying Ligands from Combinatorial Libraries. *Ann. Reports in Med. Chem.* 31:319.

- ²¹ Pomerantz, S.C., McCloskey, J.A., Eaton, B.C., 1997. Deconvolution of Combinatorial Oligonucleotide Libraries by Electrospray Ionization Tandem Mass Spectrometry. *J. Am. Chem. Soc.* 119: 3861.
- ²² Carr, S.A., Benkovic, S.J., Winograd, N. 1996. Evaluation of Mass Spectrometric Methods Applicable to the Direct Analysis of Non-Peptide Bead-Bound Combinatorial Libraries. *Anal. Chem.* 68: 237.
- ²³ Uhlen, M. et al. 1988, *Nucleic Acids Res.* 16, 3025-3038.
- ²⁴ Chrisey, L.A., Lee, G.U. and O'Ferrall, C.E. 1996. Covalent attachment of synthetic DNA to self-assembled monolayer films. *Nucleic Acids Res.* 24: 3031-3039.
- ²⁵ Timofeev, E.N., Kochetkova, S.V., Mirzabekov, A.D. and Florentiev, V.L. 1996. Regioselective immobilization of short oligonucleotides to acrylic copolymer gels. *Nucleic Acids Res.* 24: 3142-3148.
- ²⁶ O'Donnell, M.J., Tang, K., Köster, H., Smith, C.L. and Cantor, C.R. 1997. High-density, covalent attachment of DNA to silicone wafers for analysis by MALDI-TOF mass spectrometry. *Anal. Chem.* 69: 2438-2443.
- ²⁷ Cantor, C.R. 1995. Methods of preparing probe array by hybridization. US Patent. 5,631,134.
- ²⁸ Bruick, R.K., Koppitz, M., Joyce, G.F. and Orgel, L.E. 1997. A simple procedure for constructing 5'-amino-terminated oligodeoxynucleotides in aqueous solution. *Nucleic Acids Res.* 25: 1309-1310.
- ²⁹ Hockensmith, J.W., Kubasek, W.L., Vorachek, W.R. and von Hippel, P.H. 1993. Laser cross-linking of proteins to nucleic acids. *J. Bio. Chem.* 268: 15712-15720.
- ³⁰ von Hippel, P.H. 1994. Protein-DNA recognition: New perspectives and underlying themes. *Science.* 263: 769-770.

VOSSIUS & PARTNER

Patentanwälte

SIEBERTSTRASSE 4 · 81675 MÜNCHEN

TEL.: +49-89-41 30 40 · FAX: +49-89-41 30 41 11 · FAX (Marken-Trademarks): +49-89-41 30 44 00

Translation of the amended claims

1. Method for detecting a nucleotide sequence in a nucleic acid molecule comprising the following steps:
 - (a) hybridization of nucleic acid molecules to a set of probes of different nucleobase sequences, wherein each probe has a mass that differs from the one of all the other probes;
 - (b) separation of the probes that were not hybridized;
 - (c) detachment of a specifically hybridized probe in a solvent;
 - (d) analysis of the hybridized probes in a solution by means of electrospray mass spectrometry; and
 - (e) determination of the nucleic acid molecules by means of the probes hybridized to them.
2. Method according to claim 1, wherein the nucleic acid molecules are immobilized at the surface of a support before or after step (a).
3. Method according to claim 2, wherein the immobilization of the nucleic acid molecules at the surface is carried out via an NH_2 , epoxy or SH function by means of coating the surface of the probe supports with a silicate or silane, via a protein-substrate, protein-protein or a protein-nucleic acid interaction or via an interaction of two hydrophobic building blocks.
4. Method according to claim 3, wherein the protein-substrate interaction is a biotin-streptavidin bond or an antibody-antigen bond.
5. Method according to claim 3, wherein the protein-nucleic acid interaction is a Gene32-nucleic acid bond.
6. Method according to any one of claims 1 to 5, wherein the probes are nucleic acids having a mass tag.

7. Method according to claim 6, wherein the mass tag is at the same time a charge tag.
8. Method according to claim 6, wherein the nucleic acids moreover have a charge tag.
9. Method according to any one of claims 1 to 8, wherein the probes are modified nucleic acid molecules.
10. Method according to claim 9, wherein the modified nucleic acid molecules are PNAs, alkylated phosphorothioate nucleic acids or alkylphosphonate nucleic acids.
11. Method according to any one of claims 1 to 10, wherein the probes are generated by means of combinatorial solid phase synthesis.
12. Method according to claim 11, wherein different base building blocks are labelled in such a way that the probes synthesized therefrom can be differentiated in the mass spectrometer due to their mass.
13. Method according to claim 12, wherein the labelling is a methyl, ethyl, propyl, a branched or non-branched alkyl, a halogen substituted branched or non-branched alkyl, alkoxyalkyl, alkylaryl, arylalkyl, alkoxyaryl or aryloxyalkyl group or one of their deuterated or other isotopic variants.
14. Method according to any one of claims 10 to 13, wherein the probes have at least one modification in a defined position away from randomized nucleotides allowing for the cleavage of the probe.
15. Method according to claim 14, wherein modification means the introduction of a phosphorothioate group and/or an RNA base and/or a phosphotriester bond into the probe.

16. Method according to any one of claims 1 to 15, wherein the probes are generated as partial libraries having different mass and/or charge tags.
17. Method according to any one of claims 1 to 16, wherein the positions of the probes on the probe support allow for an allocation to the nucleic acid molecules hybridizing thereto.
18. Kit comprising
 - (a) a set of probes as defined in any one of claims 6 to 16 and/or
 - (b) a probe support which has been pretreated and thus allows for the attachment of target DNAs and/or target DNAs that have already been attached.

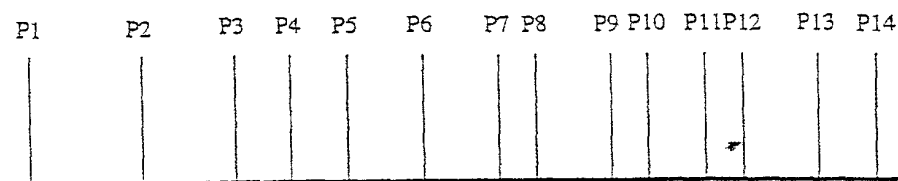
Abstract

The present invention relates to a method for detecting a nucleotide sequence in a nucleic acid molecule by means of predetermined probes with different mass using electrospray mass spectrometry. Advantageously, the method of the invention allows at the same time for the characterisation of a variety of unknown nucleic acid molecules by means of different probes. Moreover, the invention relates to a kit comprising the probes and/or a probe support, optionally with nucleic acid molecules attached thereto.

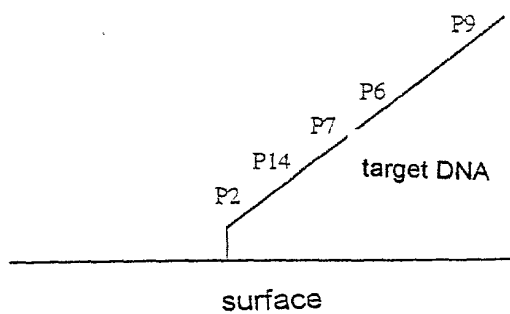
✱

004477-1 4400 006699-1 4400

1. Mass distribution of the probes



2. Hybridization



3. Mass distribution of the hybridized probes

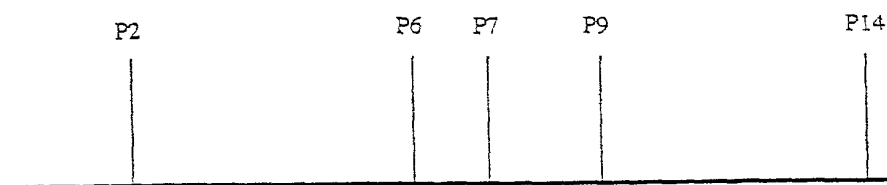
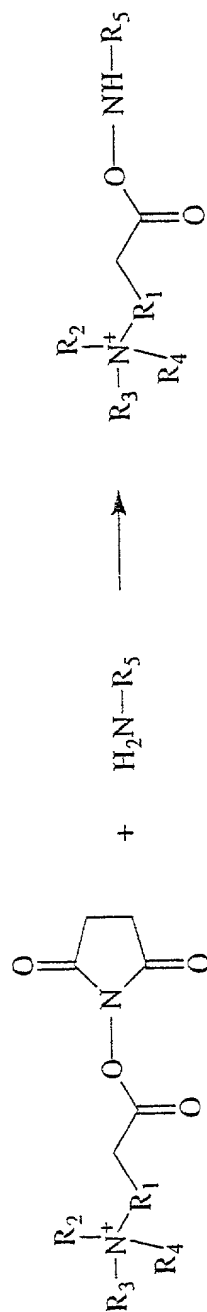


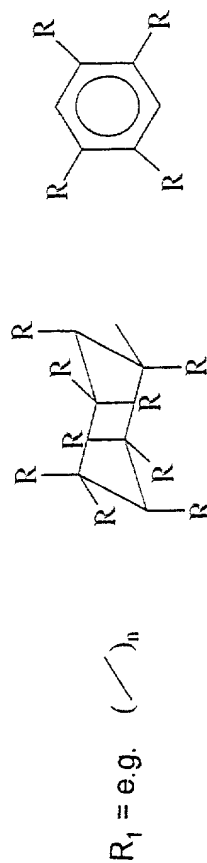
Fig. 1

N-terminal mass/charge tagging

Fig. 2



R = e.g. alkyl, -CH₃, -C₂H₅, -C₃H₇, -C₄H₉ etc.



R_{2,4} = e.g. alkyl, substituted alkyl

R₅ = e.g. nucleic acid, PNA, methyl phosphonate nucleic acid, phosphorothioate nucleic acid

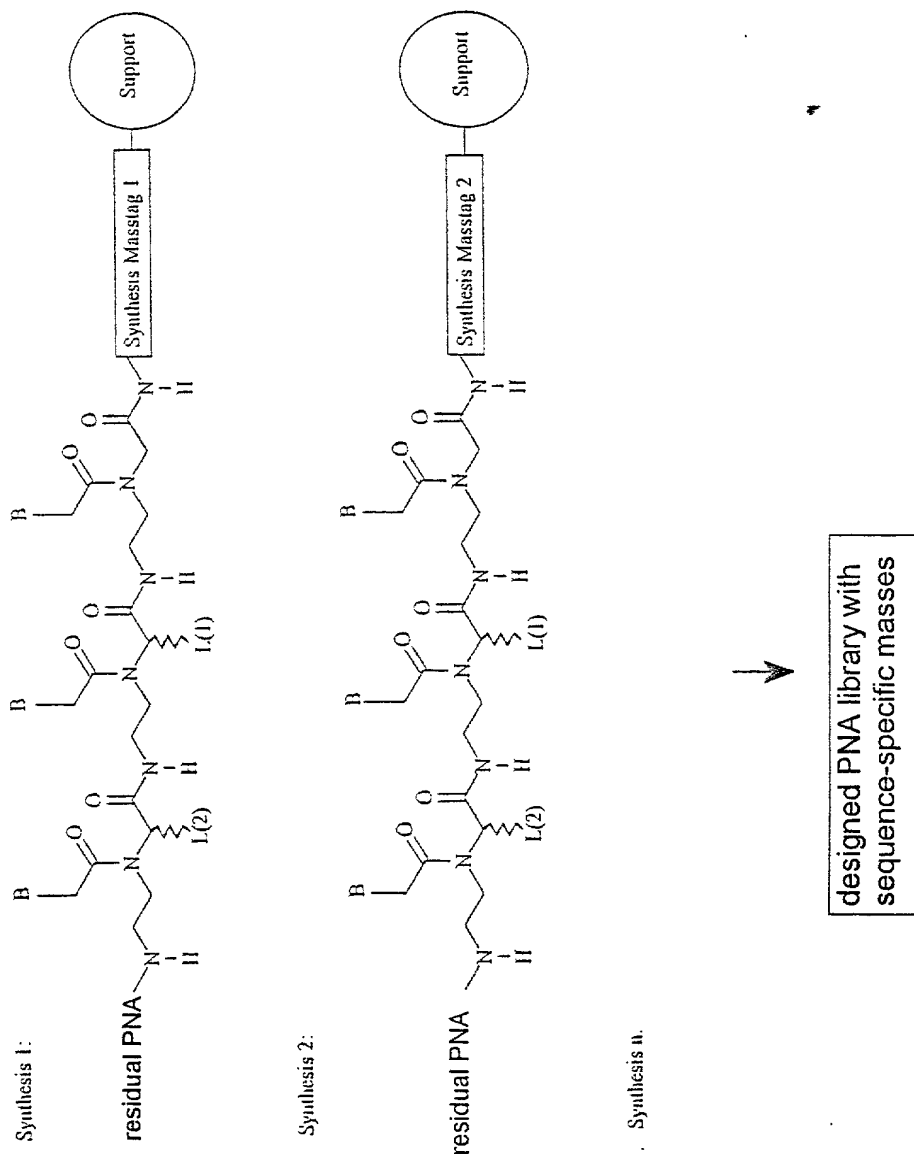


Fig. 3

B = adenine, cytosine, guanine, thymine or purine or pyrimidine derivatives or their deaza analogues

L(n) are various sets of substituents, selected specifically for each base, which are inserted in each synthesis step in order to obtain minimized peak overlaps in the MALDI-MS.

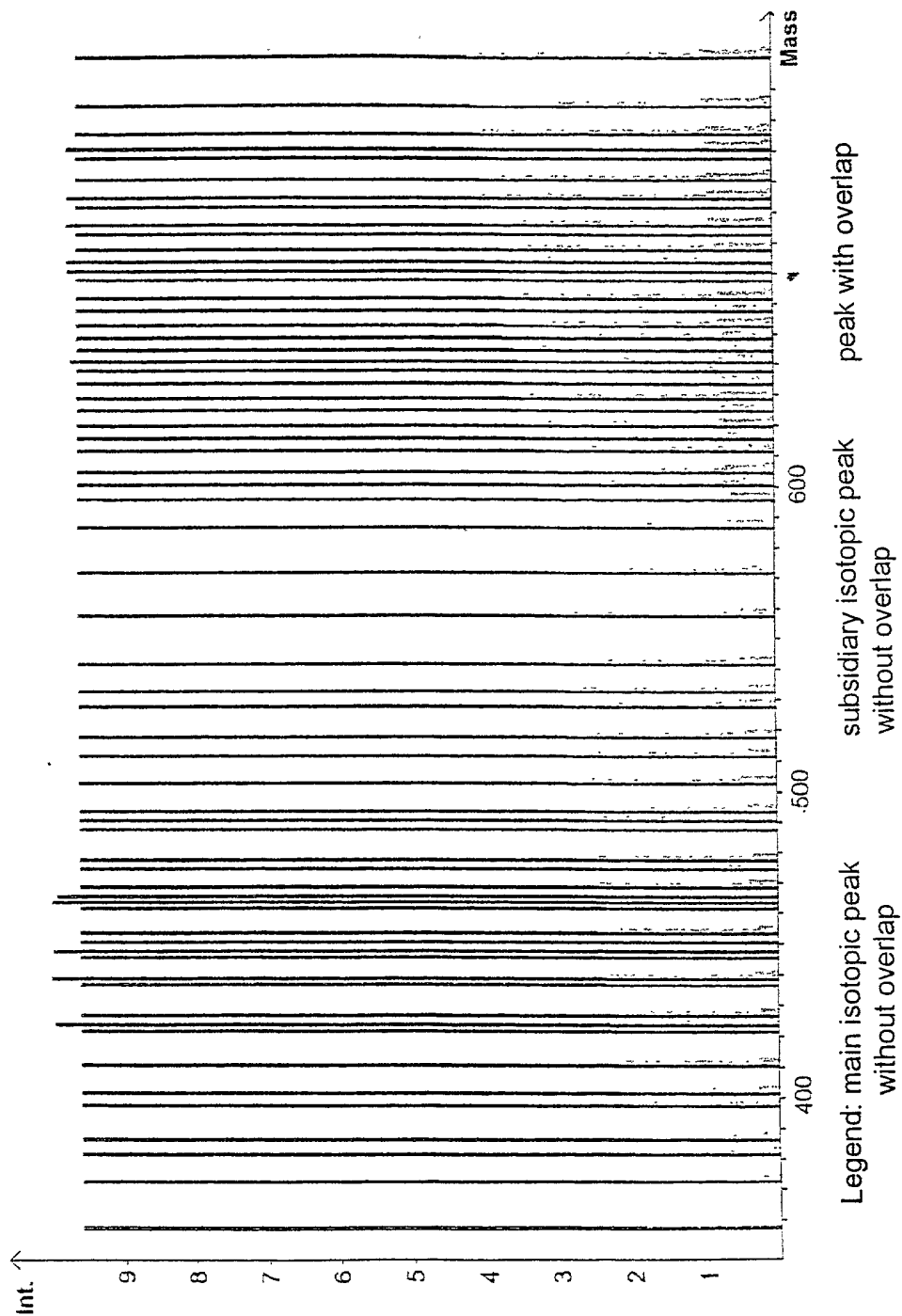


Fig. 4

64 mass peaks corresponding to a specific PNA sequence;
mass tagging

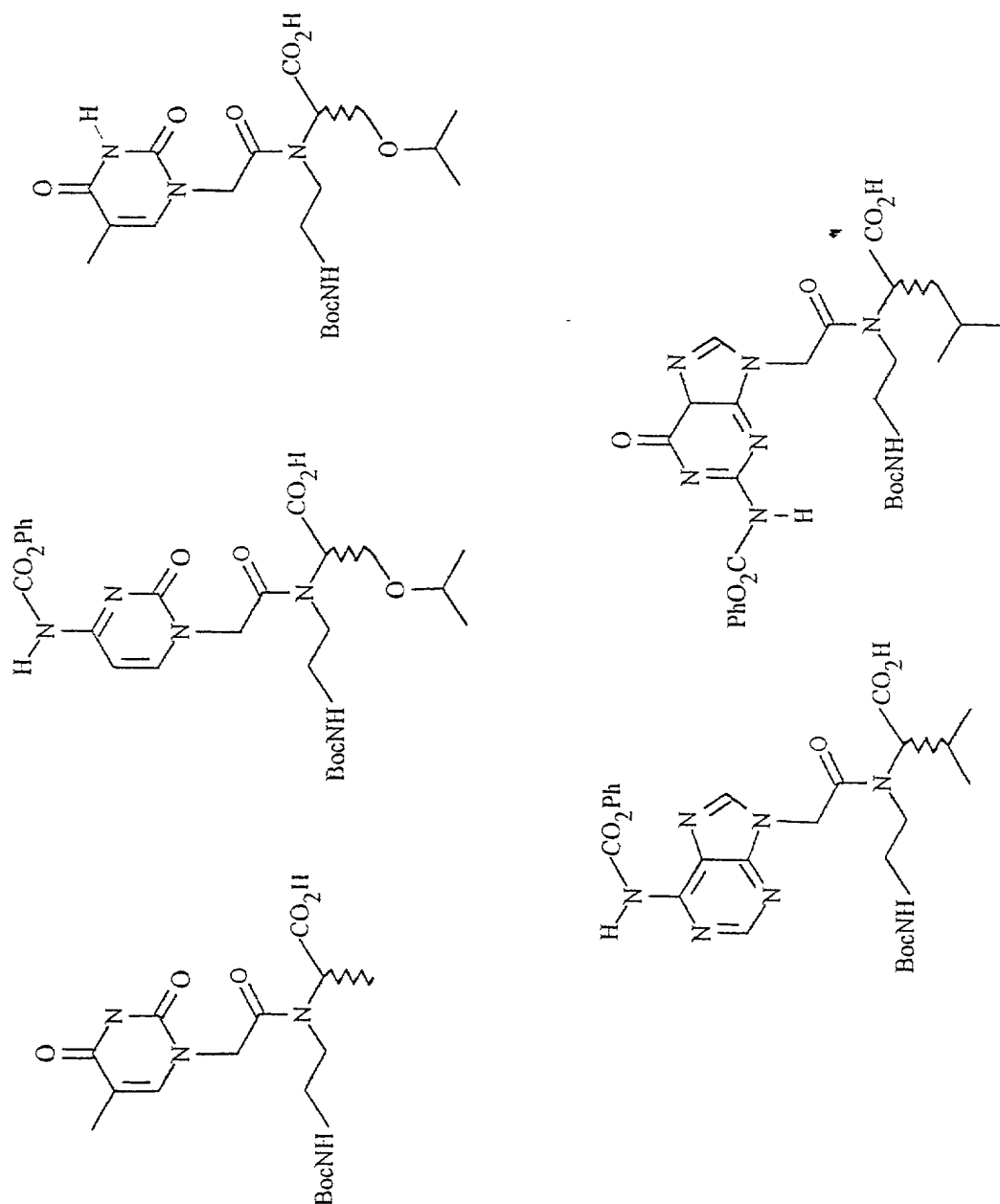


Fig. 5

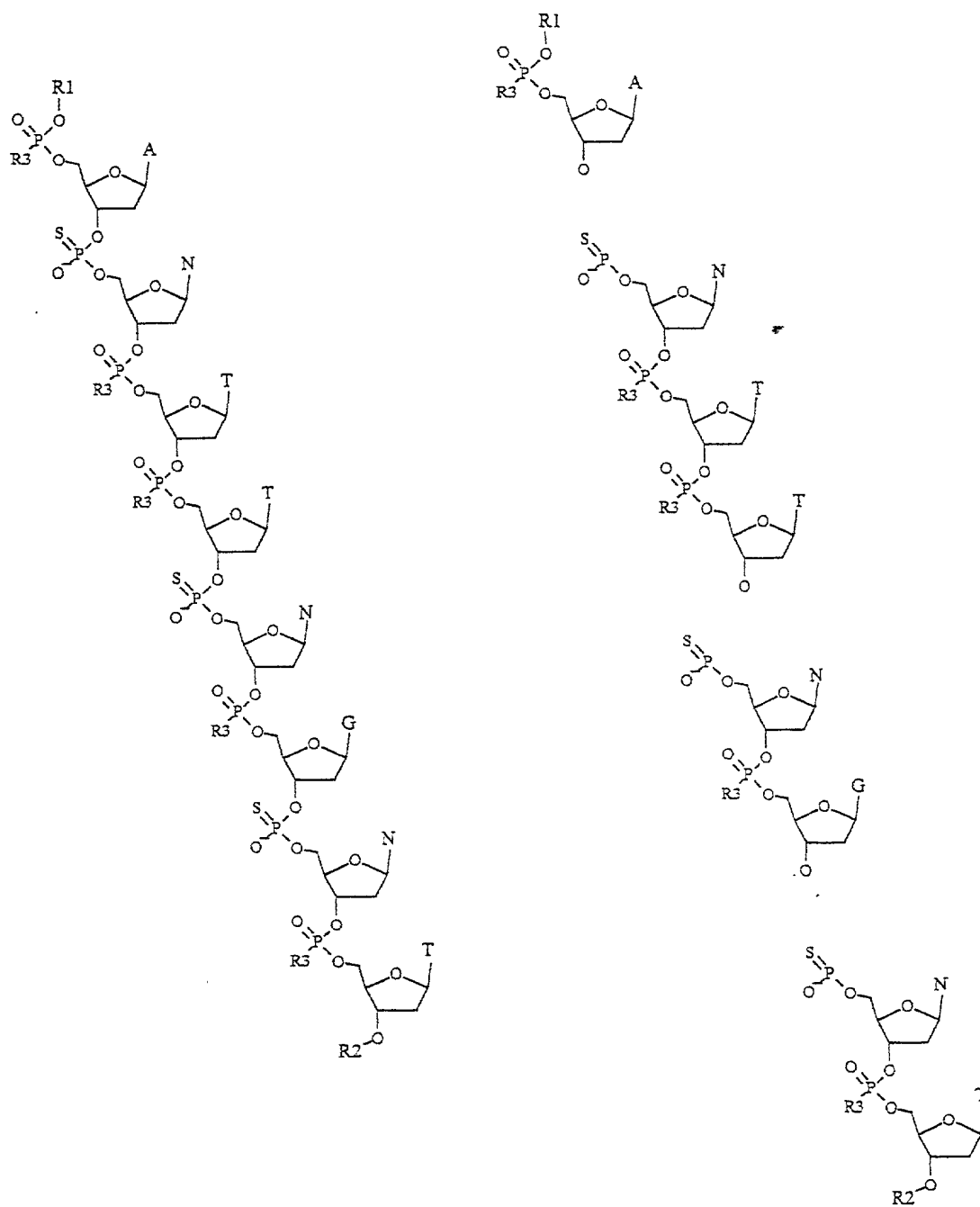


Fig. 6

B22:41

BIRCH, STEWART, KOLASCH & BIRCH, LLP

P.O. Box 747 • Falls Church, Virginia 22040-0747
Telephone: (703) 205-8000 • Facsimile: (703) 205-8050

PLEASE NOTE:
YOU MUST
COMPLETE THE
FOLLOWING

COMBINED DECLARATION AND POWER OF ATTORNEY
FOR PATENT AND DESIGN APPLICATIONS

As a below named inventor, I hereby declare that: my residence, post office address and citizenship are as stated next to my name; that I verily believe that I am the original, first and sole inventor (if only one inventor is named below) or an original, first and joint inventor (if plural inventors are named below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

Insert Title:

METHOD FOR IDENTIFYING NUCLEIC ACIDS BY ELECTRO-SPRAY MASS SPECTROMETRY

Fill in Appropriate
Information -
For Use Without
Specification
Attached:

the specification of which is attached hereto. If not attached hereto,

the specification was filed on June 5, 2000 as
United States Application Number 09/555,971;
and amended on _____ (if applicable) and/or
the specification was filed on December 4, 1998 as PCT
International Application Number PCT/EP98/07909;
amended under PCT Article 19 on _____ (if applicable)

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

I do not know and do not believe the same was ever known or used in the United States of America before my or our invention thereof, or patented or described in any printed publication in any country before my or our invention thereof or more than one year prior to this application, that the same was not in public use or on sale in the United States of America more than one year prior to this application, that the invention has not been patented or made the subject of an inventor's certificate issued before the date of this application in any country foreign to the United States of America on an application filed by me or my legal representative or assigns more than twelve months (six months for designs) prior to this application, and that no application for patent or inventor's certificate on this invention has been filed in any country foreign to the United States of America prior to this application by me or my legal representatives or assigns, except as follows.

I hereby claim foreign priority benefits under Title 35, United States Code, §119(a)-(d) of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

Prior Foreign Application(s)

Priority Claimed

Insert Priority
Information:
(if appropriate)

<u>97121470.5</u> (Number)	<u>European Patent</u> (Country)	<u>December 5, 1997</u> (Month/Day/Year Filed)	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
<u>97121983.7</u> (Number)	<u>European Patent</u> (Country)	<u>December 12, 1997</u> (Month/Day/Year Filed)	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
_____ (Number)	_____ (Country)	_____ (Month/Day/Year Filed)	<input type="checkbox"/> Yes	<input type="checkbox"/> No
_____ (Number)	_____ (Country)	_____ (Month/Day/Year Filed)	<input type="checkbox"/> Yes	<input type="checkbox"/> No

I hereby claim the benefit under Title 35, United States Code, §119(e) of any United States provisional applications(s) listed below.

Insert Provisional
Application(s):
(if any)

_____ (Application Number)	_____ (Filing Date)
_____ (Application Number)	_____ (Filing Date)

All Foreign Applications, if any, for any Patent or Inventor's Certificate Filed More than 12 Months (6 Months for Designs) Prior to the Filing Date of This Application:

Country	Application Number	Date of Filing (Month/Day/Year)
---------	--------------------	---------------------------------

Insert Requested
Information:
(if appropriate)

_____	_____	_____
_____	_____	_____

I hereby claim the benefit under Title 35, United States Code, §120 of any United States and/or PCT application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States and/or PCT application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose information which is material to the patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application.

Insert Prior U.S.
Application(s):
(if any)

_____ (Application Number)	_____ (Filing Date)	_____ (Status - patented, pending, abandoned)
_____ (Application Number)	_____ (Filing Date)	_____ (Status - patented, pending, abandoned)

I hereby appoint the following attorneys to prosecute this application and/or an international application based on this application and to transact all business in the Patent and Trademark Office connected therewith and in connection with the resulting patent based on instructions received from the entity who first sent the application papers to the attorneys identified below, unless the inventor(s) or assignee provides said attorneys with a written notice to the contrary:

Raymond C. Stewart	(Reg. No. 21,066)	Terrell C. Birch	(Reg. No. 19,382)
Joseph A. Kolasch	(Reg. No. 22,463)	James M. Slattery	(Reg. No. 28,380)
Bernard L. Sweeney	(Reg. No. 24,448)	Michael K. Mutter	(Reg. No. 29,680)
Charles Gorenstein	(Reg. No. 29,271)	Gerald M. Murphy, Jr.	(Reg. No. 28,977)
Leonard R. Svensson	(Reg. No. 30,330)	Terry L. Clark	(Reg. No. 32,644)
Andrew D. Meikle	(Reg. No. 32,868)	Marc S. Weiner	(Reg. No. 32,181)
Joe McKinney Muncy	(Reg. No. 32,334)	Donald J. Daley	(Reg. No. 34,313)
John W. Bailey	(Reg. No. 32,881)	John A. Castellano	(Reg. No. 35,094)
Gary D. Yacura	(Reg. No. 35,416)		

Send Correspondence to:

BIRCH, STEWART, KOLASCH & BIRCH, LLP

P.O. Box 747 • Falls Church, Virginia 22040-0747

Telephone: (703) 205-8000 • Facsimile: (703) 205-8050

or

Customer No. 2292

PLEASE NOTE:

**YOU MUST
COMPLETE
THE
FOLLOWING:**

Full Name of First
or Sole Inventor
Insert Name of
Inventor
Insert Date This
Document is Signed

Insert Residence
Insert Citizenship

Insert Post Office
Address

Full Name of Second
Inventor, if any
see above

Full Name of Third
Inventor, if any
see above

Full Name of Fourth
Inventor, if any
see above

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

GIVEN NAME/FAMILY NAME <u>Ivo Glynne GUT</u>		INVENTOR'S SIGNATURE <u>Ivo Glynne Gut</u>	DATE* <u>3. October 2000</u>
Residence (City, State & Country) <u>Paris, France</u> FRX		CITIZENSHIP <u>Swiss/British</u>	
POST OFFICE ADDRESS (Complete Street Address including City, State & Country) <u>18 rue du Moulin Vert, 75014 Paris, France</u>			
GIVEN NAME/FAMILY NAME <u>Kurt BERLIN</u>		INVENTOR'S SIGNATURE <u>Kurt Berlin</u>	DATE* <u>3. October 2000</u>
Residence (City, State & Country) <u>Stahnsdorf, Germany</u> DEX		CITIZENSHIP <u>German</u>	
POST OFFICE ADDRESS (Complete Street Address including City, State & Country) <u>Marienkaferweg 4, 14532 Stahnsdorf, Germany</u>			
GIVEN NAME/FAMILY NAME <u>Hans LEHRACH</u>		INVENTOR'S SIGNATURE <u>Hans Lehrach</u>	DATE* <u>3. October 2000</u>
Residence (City, State & Country) <u>Berlin, Germany</u> DEX		CITIZENSHIP <u>Austrian</u>	
POST OFFICE ADDRESS (Complete Street Address including City, State & Country) <u>Lutzelsteinerweg 50, 14195 Berlin, Germany</u>			
GIVEN NAME/FAMILY NAME		INVENTOR'S SIGNATURE	DATE*
Residence (City, State & Country)		CITIZENSHIP	
POST OFFICE ADDRESS (Complete Street Address including City, State & Country)			

*DATE OF SIGNATURE

I hereby appoint the following attorneys to prosecute this application and/or an international application based on this application and to transact all business in the Patent and Trademark Office connected therewith and in connection with the resulting patent based on instructions received from the entity who first sent the application papers to the attorneys identified below, unless the inventor(s) or assignee provides said attorneys with a written notice to the contrary:

Raymond C. Stewart	(Reg. No. 21,066)	Terrell C. Birch	(Reg. No. 19,382)
Joseph A. Kolasch	(Reg. No. 22,463)	James M. Slattery	(Reg. No. 28,380)
Bernard L. Sweeney	(Reg. No. 24,448)	Michael K. Mutter	(Reg. No. 29,680)
Charles Gorenstein	(Reg. No. 29,271)	Gerald M. Murphy, Jr.	(Reg. No. 28,977)
Leonard R. Svensson	(Reg. No. 30,330)	Terry L. Clark	(Reg. No. 32,644)
Andrew D. Meikle	(Reg. No. 32,868)	Marc S. Weiner	(Reg. No. 32,181)
Joe McKinney Muncy	(Reg. No. 32,334)	Donald J. Daley	(Reg. No. 34,313)
John W. Bailey	(Reg. No. 32,881)	John A. Castellano	(Reg. No. 35,094)
Gary D. Yacura	(Reg. No. 35,416)		

Send Correspondence to:

BIRCH, STEWART, KOLASCH & BIRCH, LLP

or

Customer No. 2292

P.O. Box 747 • Falls Church, Virginia 22040-0747

Telephone: (703) 205-8000 • Facsimile: (703) 205-8050

PLEASE NOTE:

**YOU MUST
COMPLETE
THE
FOLLOWING:**



Full Name of First
or Sole Inventor
Insert Name of
Inventor →
Insert Date This
Document is Signed

Insert Residence
Insert Citizenship →

Insert Post Office
Address →

Full Name of Second
Inventor, if any
see above

Full Name of Third
Inventor, if any
see above

Full Name of Fourth
Inventor, if any
see above

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

GIVEN NAME/FAMILY NAME		INVENTOR'S SIGNATURE	DATE*
Ivo Glynne GUT			00/10/30
Residence (City, State & Country)		CITIZENSHIP	
Paris, France		Swiss/British	
POST OFFICE ADDRESS (Complete Street Address including City, State & Country)			
18 rue du Moulin Vert, 75014 Paris, France			
GIVEN NAME/FAMILY NAME		INVENTOR'S SIGNATURE	DATE*
Kurt BERLIN			00/10/30
Residence (City, State & Country)		CITIZENSHIP	
Stahnsdorf, Germany		German	
POST OFFICE ADDRESS (Complete Street Address including City, State & Country)			
Marienkaferweg 4, 14532 Stahnsdorf, Germany			
GIVEN NAME/FAMILY NAME		INVENTOR'S SIGNATURE	DATE*
Hans LEHRACH			
Residence (City, State & Country)		CITIZENSHIP	
Berlin, Germany		Austrian	
POST OFFICE ADDRESS (Complete Street Address including City, State & Country)			
Lutzelsteinerweg 50, 14195 Berlin, Germany			
GIVEN NAME/FAMILY NAME		INVENTOR'S SIGNATURE	DATE*
Residence (City, State & Country)		CITIZENSHIP	
POST OFFICE ADDRESS (Complete Street Address including City, State & Country)			

I hereby appoint the following attorneys to prosecute this application and/or an international application based on this application and to transact all business in the Patent and Trademark Office connected therewith and in connection with the resulting patent based on instructions received from the entity who first sent the application papers to the attorneys identified below, unless the inventor(s) or assignee provides said attorneys with a written notice to the contrary:

Raymond C. Stewart	(Reg. No. 21,066)	Terrell C. Birch	(Reg. No. 19,382)
Joseph A. Kolasch	(Reg. No. 22,463)	James M. Slattery	(Reg. No. 28,380)
Bernard L. Sweeney	(Reg. No. 24,448)	Michael K. Mutter	(Reg. No. 29,680)
Charles Gorenstein	(Reg. No. 29,271)	Gerald M. Murphy, Jr.	(Reg. No. 28,977)
Leonard R. Svensson	(Reg. No. 30,330)	Terry L. Clark	(Reg. No. 32,644)
Andrew D. Meikle	(Reg. No. 32,868)	Marc S. Weiner	(Reg. No. 32,181)
Joe McKinney Muncy	(Reg. No. 32,334)	Donald J. Daley	(Reg. No. 34,313)
John W. Bailey	(Reg. No. 32,881)	John A. Castellano	(Reg. No. 35,094)
Gary D. Yacura	(Reg. No. 35,416)		

Send Correspondence to:

BIRCH, STEWART, KOLASCH & BIRCH, LLP

or

Customer No. 2292

P.O. Box 747 • Falls Church, Virginia 22040-0747

Telephone: (703) 205-8000 • Facsimile: (703) 205-8050

PLEASE NOTE:

**YOU MUST
COMPLETE
THE
FOLLOWING:**



Full Name of First
or Sole Inventor.
Insert Name of
Inventor
Insert Date This
Document is Signed



Insert Residence
Insert Citizenship



Insert Post Office
Address

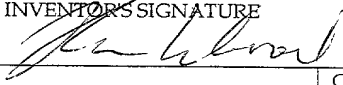


Full Name of Second
Inventor, if any.
see above

Full Name of Third
Inventor, if any
see above

Full Name of Fourth
Inventor, if any
see above

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

GIVEN NAME/FAMILY NAME		INVENTOR'S SIGNATURE		DATE*	
Ivo Glynne GUT					
Residence (City, State & Country)				CITIZENSHIP	
Paris, France				Swiss/British	
POST OFFICE ADDRESS (Complete Street Address including City, State & Country)					
18 rue du Moulin Vert, 75014 Paris, France					
GIVEN NAME/FAMILY NAME		INVENTOR'S SIGNATURE		DATE*	
Kurt BERLIN					
Residence (City, State & Country)				CITIZENSHIP	
Stahnsdorf, Germany				German	
POST OFFICE ADDRESS (Complete Street Address including City, State & Country)					
Marienkaferweg 4, 14532 Stahnsdorf, Germany					
GIVEN NAME/FAMILY NAME		INVENTOR'S SIGNATURE		DATE*	
Hans LEHRACH				1 Nov 2000	
Residence (City, State & Country)				CITIZENSHIP	
Berlin, Germany				Austrian	
POST OFFICE ADDRESS (Complete Street Address including City, State & Country)					
Kuxsdenweg 58, 11098 Berlin, Germany Terrassenstrasse 31, 14129 Berlin, Germany					
GIVEN NAME/FAMILY NAME		INVENTOR'S SIGNATURE		DATE*	
Residence (City, State & Country)				CITIZENSHIP	
POST OFFICE ADDRESS (Complete Street Address including City, State & Country)					

*DATE OF SIGNATURE